

REPLACEMENT SHEET



SEQ ID 2 1 ATG TTG CAG ATG GCT GGG CAG TGC TCC CAA AAT GAA TAT TTT GAC AGT TTG TTG CAT GCT
 SEQ ID 1 1▶ M L Q M A G Q C S Q N E Y F D S L L L H A
 61 TGC ATA CCT TGT CAA CTT OGA TGT TCT TCT AAT ACT CCT OCT CTA ACA TGT CAG CGT TAT
 21▶ C I P C Q L R C S S N T P P L T C Q R Y
 121 TGT AAT GCA AGT GTG ACC AAT TCA GTG AAA GGA ACG AAT GCG ATT CTC TGG ACC TGT TTG
 41▶ C N A S V T N S V K G T N A I L W T C L
 181 GGA CTG AGC TTA ATA ATT TCT TTG GCA GTT TTC GTG CTA ATG TTT TTG CTA AGG AAG ATA
 61▶ G L S L I I S L A V F V L M F L L R K I
 241 AGC TCT GAA OCA TTA AAG GAC GAG TTT AAA AAC ACA GGA TCA GGT CTC CTG GGC ATG GCT
 81▶ S S E P L K D E F K N T G S G L L G M A
 301 AAC ATT GAC CTG GAA AAG AGC AGG ACT GGT GAT GAA ATT ATT CTT OCG AGA GGC CTC GAG
 101▶ N I D L E K S R T G D E I L P R G L E
 361 TAC ACG GTG GAA GAA TGC ACC TGT GAA GAC TGC ATC AAG AGC AAA CCG AAG GTC GAC TCT
 121▶ Y T V E E C T C E D C I K S K P K V D S
 421 GAC CAT TGC TTT OCA CTC OCA GCT ATG GAG GAA GGC GCA ACC ATT CTT GTC ACC ACG AAA
 141▶ D H C F P L P A M E G A T I L V T T K
 481 ACG AAT GAC TAT TGC AAG AGC CTG OCA GCT GCT TTG AGT GCT ACG GAG ATA GAG AAA TCA
 161▶ T N D Y C K S L P A A L S A T E I E K S
 541 ATT TCT GCT AGG TAA
 181▶ I S A R .

FIG. 1

REPLACEMENT SHEET

SEQ ID NO:8

1 AAGACTCAAA CTTAGAACT TGAATTAGAT GTGGTATTCA AATCCTTACG TGCOCGGAAG
61 ACACAGACAG CCCCCGTAAG AACCCAAGAA GCAGGCGAAG TTCATTGTTT TCAACATTCT

EcoRI

121 AGCTGCTCTT GCTGCATTTG CTCTGGAATT CTTGTAGAGA TATTACTTGT CCTTCCAGGC

SfiI

BclI

181 TGTCTTTTCT GTAGCTCCCT TGTCTTCTTT TGTGATCAT GTTGCAGATG GCTGGGCAGT

SEQ ID NO:1 1► M L Q M A G Q

SspI

SphI

HincII

241 GCTCCCAAAA TGAATATTTT GACAGTTTGT TGCATGCTTG CATACCTTGT CAACTTCGAT

8► C S Q N E Y F D S L L H A C I P C Q L R

PciI

AflIII

301 GTTCTTCTAA TACTCCTCCT CTAACATGTC AGCGTTATTG TAATGCAAGT GTGACCAATT

28► C S S N T P P L T C Q R Y C N A S V T N

BsmFI

361 CAGTGAAAGG AACGAATGCG ATTCTCTGGA CCTGTTTGGG ACTGAGCTTA ATAATTTCTT

48► S V K G T N A I L W T C L G L S L I I S

421 TGGCAGTTT CGTGCTAATG TTTTGTCTAA GGAAGATAAG CTCTGAACCA TTAAAGGACG

68► L A V F V L M F L L R K I S S E P L K D

DraI

AluI

BsaI

481 AGTTTAAAAA CACAGGATCA GGTCTCCTGG GCATGGCTAA CATTGACCTG GAAAAGAGCA

88► E F K N T G S G L L G M A N I D L E K S

XmnI

StuI XhoI

541 GGAAGTGGTA TGAAATTATT CTTCCGAGAG GCCTCGAGTA CACGGTGGAA GAATGCACCT

108► R T G D E I I L P R G L E Y T V E E C T

Sall

HincII

AccI

BbsI

601 GTGAAGACTG CATCAAGAGC AAACCGAAGG TCGACTCTGA CCATTGCTTT CCACTCCCAG

128► C E D C I K S K P K V D S D H C F P L P

661 CTATGGAGGA AGGCGCAACC ATTCTTGTCA CCACGAAAAC GAATGACTAT TGCAAGAGCC

148► A M E E G A T I L V T T K T N D Y C K S

PvuII

721 TGCCAGCTGC TTTGAGTGCT ACGGAGATAG AGAAATCAAT TTCTGCTAGG TAATTAACCA

168► L P A A L S A T E I E K S I S A R

XhoI

DraI

BglII

781 TTTCGACTCG AGCAGTGCCA CTTTAAAAAT CTTTGTTCAG AATAGATGAT GTGTCAGATC

841 TCTTTAGGAT GACTGTATTT TTCAGTTGCC GATACAGCTT TTTGTCCTCT AACTGTGGAA

StyI

901 ACTCTTTATG TTAGATATAT TTCTCTAGGT TACTGTTGGG AGCTTAATGG TAGAACTTC

961 CTTGGTTTCA TGATTAAAGT CTTTTTTTTT CCTGA

FIG. 3

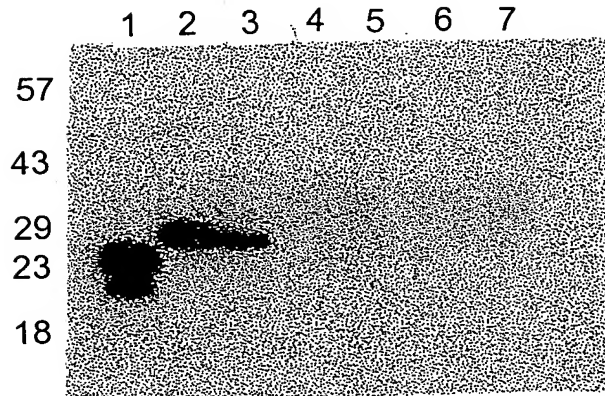


FIG. 7

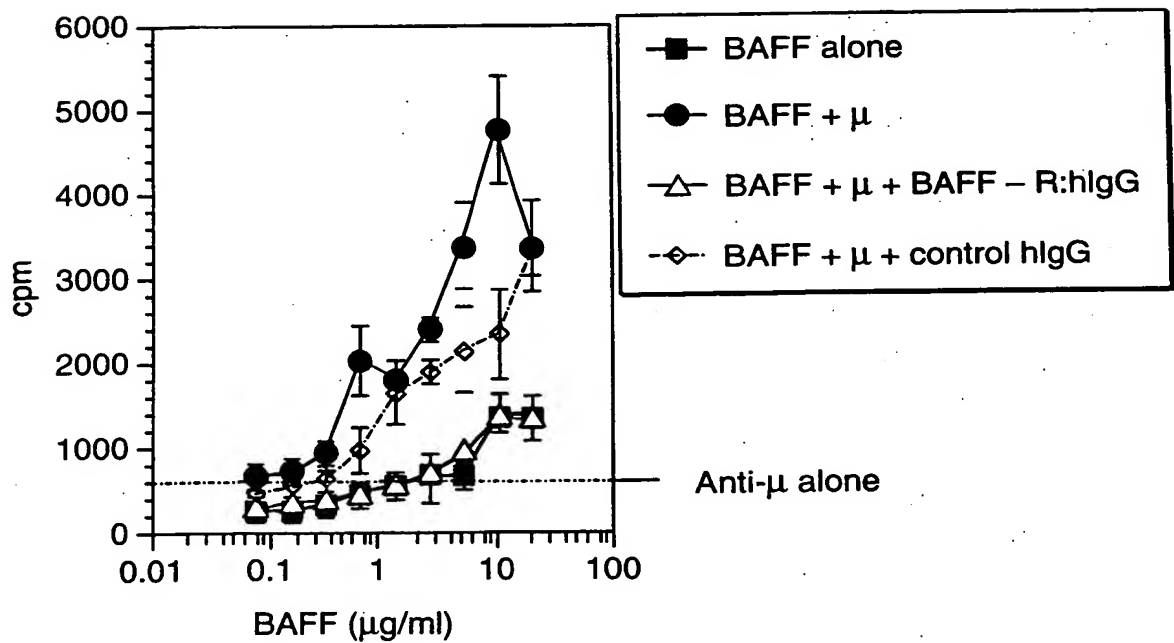


FIG. 8